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- 1 -

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

~~<120> NOVEL GENETIC SEQUENCES ENCODING STEROID AND JUVENILE HORMONE~~

5 RECEPTOR POLYPEPTIDES AND INSECTICIDAL MODALITIES THEREFOR II

<130> p:\oper\mro\ecdysone.cip

<140> US continuation-in-part of PCT/AU99/00033

<141> 1999-07-02

10 <150> PCT/AU/00033

<151> 1999-01-15

<150> AU PP1536

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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- 3 -

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	His Asn His Leu His His Asn Ser Asn Ser Asn His Ser Asn Ser Ser	
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	tta tcg gtc aat att aat ggt ccc aat atc gtt agc aat gcc caa cag	624
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	210 215 220	
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	Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His His	
	225 230 235 240	
25	cat cat atg aat aac agt agt atg atg cat cat aca ccc aga tct gaa	768
	His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu	
	245 250 255	
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30	Ser Ala Asn Ser Ile Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser	
	260 265 270	

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 Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys
 370 375 380

[illegible]

- 6 -

525

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- 7 -

caa tcg gat aat gca tag 2274

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35 40 45

Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr

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20

Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr

65 70 75 80

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30 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val
115 120 125

- 9 -

Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys

Abstract

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- 11 -

Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp

465

470

475

480

Ala Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu

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490

495

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln

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510

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Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met

515

520

525

Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe

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530

535

540

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met

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550

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560

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Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ser

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570

575

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile

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585

590

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Phe Ser Asp Arg Pro Gly Leu Glu Glu Ala Glu Leu Val Glu Ala Ile

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605

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His

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667020"0437E60

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<213> Lucillia cuprina

P:OPER\MRO\ECDYSONE,CIP-17

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<222> (1)..(1401)

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- 16 -

Abstract—The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The children were divided into two groups: a control group and an experimental group. The experimental group participated in a 12-week training program that included aerobic, strength, and flexibility exercises. The control group did not participate in any training program. Physical fitness was measured at the beginning and end of the 12-week period using a series of tests including a 1000-meter run, a 1-minute sit-up test, a 1-minute plank test, a 1-minute push-up test, a 1-minute side plank test, a 1-minute leg lift test, a 1-minute arm lift test, a 1-minute core stability test, a 1-minute balance test, a 1-minute coordination test, a 1-minute reaction time test, a 1-minute speed test, a 1-minute agility test, a 1-minute endurance test, a 1-minute strength test, a 1-minute flexibility test, a 1-minute balance test, a 1-minute coordination test, a 1-minute reaction time test, a 1-minute speed test, a 1-minute agility test, a 1-minute endurance test, a 1-minute strength test, and a 1-minute flexibility test. The results of the study showed that the experimental group had significantly higher scores than the control group in all of the tests at the end of the 12-week period. The results also showed that the experimental group had significantly higher scores than the control group in all of the tests at the beginning of the 12-week period. The results of the study suggest that a 12-week training program can improve the physical fitness of 10-year-old children.

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25	Arg Arg Ser Pro Val Arg Gln Pro Gln Gln Leu Phe Leu Asn Gln Asn		
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- 19 -

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Tyr Lys Phe

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1. The first part of the report, "Introduction", discusses the importance of the study and the objectives of the research.

- 22 -

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6060343460

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 Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala
 35 40 45
 15
 Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala
 50 55 60
 20
 Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly
 65 70 75 80
 25
 Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
 85 90 95
 30
 Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
 100 105 110
 35
 Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
 115 120 125
 40
 Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 45
 Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
 145 150 155 160
 50
 Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
 165 170 175
 55
 Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Lys Leu Asn
 180 185 190
 60
 His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
 195 200 205
 65
 Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
 210 215 220
 70
 Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
 225 230 235 240
 75
 Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn
 245 250 255 260
 80
 85
 90

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	245					250					255						
5	Ala	Val	Tyr	Gln	Cys	Lys	Tyr	Gly	Asn	Asn	Cys	Glu	Ile	Asp	Met	Tyr	
	260					265					270						
10	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Thr	Val	
	275					280					285						
15	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Val	Gln	Cys	Ala	Val	Lys	
	290					295					300						
20	Arg	Lys	Glu	Lys	Lys	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Pro	Asn	Ser	Thr	
25	305					310					315					320	
30	Thr	Asp	Ile	Ser	Pro	Glu	Ile	Ile	Lys	Ile	Glu	Pro	Thr	Glu	Met	Lys	
	325					330					335						
35	Ile	Glu	Cys	Gly	Glu	Pro	Met	Ile	Met	Gly	Thr	Pro	Met	Pro	Thr	Val	
	340					345					350						
40	Pro	Tyr	Val	Lys	Pro	Leu	Ser	Ser	Glu	Gln	Lys	Glu	Leu	Ile	His	Arg	
	355					360					365						
45	Leu	Val	Tyr	Phe	Gln	Asp	Gln	Tyr	Glu	Ala	Pro	Ser	Glu	Lys	Asp	Met	
50	370					375					380						
55	Lys	Arg	Leu	Thr	Ile	Asn	Asn	Gln	Asn	Met	Asp	Glu	Tyr	Asp	Glu	Glu	
	385					390					395					400	
60	Lys	Gln	Ser	Asp	Thr	Thr	Tyr	Arg	Ile	Ile	Thr	Glu	Met	Thr	Ile	Leu	
	405					410					415						
65	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Arg	Leu	Pro	Gly	Phe	Asp	
	420					425					430						
70	Lys	Leu	Val	Arg	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	
	435					440					445						
75	Glu	Ala	Met	Met	Phe	Arg	Val	Ala	Arg	Lys	Tyr	Asp	Ile	Thr	Thr	Asp	
80	450					455					460						
85	Ser	Ile	Val	Phe	Ala	Asn	Asn	Gln	Pro	Phe	Ser	Ala	Asp	Ser	Tyr	Asn	
	465					470					475					480	
90	Lys	Ala	Gly	Leu	Gly	Asp	Ala	Ile	Glu	Asn	Gln	Leu	Ser	Phe	Ser	Arg	
	485					490					495						

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	50	55	60	
5	tgc gag ggg tgc aaa ggg ttc ttc aaa cgc aca gtg agg aaa aat ttg			240
	Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu			
10	65	70	75	80
15	tca tac gcg tgt cgc gaa gaa aac aaa tgc atc atc gac aag cgc caa			288
	Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln			
		85	90	95
20	cga aat cgg tgc caa tac tgc agg tat caa aaa tgt ttg acc atg ggc			336
	Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly			
25		100	105	110
30	atg aaa aga gaa gct gtg cag gaa gaa aga caa cgt aca aaa gaa cga			384
	Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg			
		115	120	125
35	gat cat aat aac atc gaa gtt gaa ccc acg agc agt tct aat act gat			432
40	Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp			
		130	135	140
45	atg cca gtg gaa ctc ata tta agg gct gag aat aaa gct gat gct ata			480
	Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile			
50	145	150	155	160
55	aag act gaa caa cag tat ata gag caa cga cat cct caa cat act gtt			528
	Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val			
		165	170	175
60	ggt gct att tgt caa gca act gac aag cag tta ata caa ctt gtc gaa			576
	Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu			
65		180	185	190
70	tgg gcc aag cat ata ccg cat ttt aaa aat tta cct cta ggc gat caa			624
	Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln			
		195	200	205
75	gtt tta tta ttg aga gct ggt tgg aat gag ttg atg att gca gca ttt			672
80	Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe			
		210	215	220
85	tcc cat aga tca atc agt gta aaa gat ggt ata gtc tta gct act gga			720
	Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly			
90	225	230	235	240

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	ctt act gtt gac aga gat tca gct cac caa gct ggt gtt gaa gct ata	768
5	Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile 245 250 255	
10	ttt gat cgt gta ctc act gaa ctc gtt gct aaa atg aga gat atg ggt Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly	816
15	260 265 270	
20	atg gat aga aca gag ctt ggc tgt ttg cgt act att att ctt ttt aat Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn	864
25	275 280 285	
30	cca ggt tca aaa ggt ttg cag tct gtg aat gaa gtg caa gta ctg cgt Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg	912
35	290 295 300	
40	gat aag gtt tac gtt gcg tta gaa gaa tat tgt cgt aca aca cat cca Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro	960
45	305 310 315 320	
50	gaa gaa cct gga cga ttt gct aaa cta ctt ctt cgg ctt cct tca tta Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu	1008
55	325 330 335	
60	cgt tca att gga tta aaa tgt ctg gaa cat tta ttc ttt tat aaa ctt Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu	1056
65	340 345 350	
70	att ggc gat tcc cca att gat aca ttt tta atg gaa gtt ctc gaa tca Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser	1104
75	355 360 365	
80	tct tca cat gac gtt caa gta gct aca Ser Ser His Asp Val Gln Val Ala Thr	1131
85	370 375	
90	<210> 12 <211> 377 <212> PRT <213> Myzus persicae <400> 12 Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser	
	1 5 10 15	

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Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
 20 25 30
 5
 Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
 35 40 45
 10
 Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser
 50 55 60
 15
 Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu
 65 70 75 80
 20
 Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln
 85 90 95
 25
 Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly
 100 105 110
 30
 Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg
 115 120 125
 35
 Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp
 130 135 140
 40
 Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile
 145 150 155 160
 45
 Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val
 165 170 175
 50
 Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu
 180 185 190
 55
 Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln
 195 200 205
 60
 Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe
 210 215 220
 65
 Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly
 225 230 235 240
 70
 Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile
 245 250 255
 75
 Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly
 80
 85
 90

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- 32 -

260 265 270

5 Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn
275 280 285

10 Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg
290 295 300

15 Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro
305 310 315 320

20 Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
325 330 335

25 Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu
340 345 350

30 Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser
355 360 365

35 Ser Ser His Asp Val Gln Val Ala Thr
370 375

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<211> 150

<212> DNA

50 <213> Lucilia cuprina

<220>

<221> CDS

<222> (9) .. (134)

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<400> 13

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Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp

1 5 10

60

ttg aca tat gct tgt cgt gag gac aga aat tgc att ata gat aaa cga 90

- 33 -

Leu Thr Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg
15 20 25 30

caa aga aat cgt tgc cag tat tgt cgc tac caa aag tgatcgatac cgtcga 150

5 Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
 35 40

<210> 14

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<213> Lucilia cuprina

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Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr

15 1 5 10 15

Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg
20 25 30

20 Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
35 40

<210> 15

25 <211> 32

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30 <223> Description of Artificial Sequence:primer

<400> 15

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5 <210> 16

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<223> Description of Artificial Sequence:primer

<400> 16

32

15

<210> 17

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25 <400> 17

23

<210> 18

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DRAFT

- 35 -

<213> Artificial Sequence

<220>

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<400> 18

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23

10

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence:primer

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23

<210> 20

<211> 24

25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

30

<400> 20

tagaccttg gcraytcna caat

24

66703044460

Sub
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cont